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Sequence Listing was accepted.

See attached Validation Report.

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217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: Tue Sep 25 13:36:29 EDT 2007

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Application No: 10594732 Version No: 1.0

Input Set:

Output Set:

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Finished: 2007-09-12 13:58:38.340
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 318 ms
Total Warnings: 14
Total Errors: 2
No. of SeqIDs Defined: 44
Actual SeqID Count: 44

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NATIONAL INSTITUTE OF TECHNOLOGY AND EVALUATION

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<130> PH-2387-PCT

<140> 10594732

<141> 2007-09-12

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<150> JP 2004-105642

<151> 2004-03-31

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<170> PatentIn Ver. 2.1

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<211> 777

<212> DNA

<213> Manihot esculenta

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<223> Inventor: Ichige, Eita; Semba, Hisashi; Shijuku, Toshiaki; Harayama, Shigeaki

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<221> CDS

<222> (1)..(777)

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180 185 190	
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Cys Gly Gly Leu Asn Ile Ala Ile Ala Ala Asp Lys Tyr Cys Glu Lys
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Ile Ala Ala Ala Val Phe His Asn Ser Val Leu Pro Asp Thr Glu His
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Cys Pro Ser Tyr Val Val Asp Lys Leu Met Glu Val Phe Pro Asp Trp
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Ser Leu Phe Gln Asn Ile Leu Ala Lys Arg Pro Phe Phe Thr Lys Glu
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Gly Tyr Gly Ser Ile Lys Lys Ile Tyr Val Trp Thr Asp Gln Asp Glu
      195            200            205
Ile Phe Leu Pro Glu Phe Gln Leu Trp Gln Ile Glu Asn Tyr Lys Pro
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tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa    96
Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
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gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc			192
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe			
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ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc			240
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser			
65	70	75	80
tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa			288
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys			
85	90	95	
att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac			336
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His			
100	105	110	
agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg			384
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp			
115	120	125	
cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc			432
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile			
130	135	140	
act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc			480
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr			
145	150	155	160
aaa tgc act gat gac gaa tat gaa ctg gca aaa atg gtt atg cgc aag			528
Lys Cys Thr Asp Asp Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys			
165	170	175	
ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa			576
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu			
180	185	190	
aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac			624
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp			
195	200	205	
aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa			672
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys			
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ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg			720
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu			
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aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca			768
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tac gct taa
Tyr Ala

777

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a replacement of Gly by Asp at position 165

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35 40 45
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50 55 60
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
65 70 75 80
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
85 90 95
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
100 105 110
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
115 120 125
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
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Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
145 150 155 160
Lys Cys Thr Asp Asp Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
165 170 175
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
180 185 190
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
195 200 205
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
210 215 220
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
225 230